

Amendments to the Claims:

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Original) A method of diagnosing a CRH induced gene expression profile in an individual said method comprising:
 - a) obtaining a biological sample of said individual; and
 - b) determine the level of gene transcription of a gene comprising a nucleic acid sequence selected from the group consisting of SEQ ID No.1, SEQ ID No.2, SEQ ID No.3, SEQ ID No.4, SEQ ID NO.5, SEQ ID NO.6, SEQ ID No.7, SEQ ID No.8, SEQ ID NO.9, SEQ ID 11, SEQ ID NO.13, SEQ ID NO.15, SEQ ID NO.17, SEQ ID NO.19, SEQ ID NO.21, SEQ ID NO.23, SEQ ID No.25, SEQ ID No.26, SEQ ID No.27, SEQ ID No.28, SEQ ID No.29, SEQ ID No.30, SEQ ID No.31, SEQ ID NO.32, SEQ ID NO.34, SEQ ID NO.36, SEQ ID No.38 and SEQ ID No.40.
2. (Currently Amended) A method according to claim 1 wherein the biological sample is a bodily fluid or tissue sample.
3. (Currently Amended) A method according to ~~claims 1 or 2~~ claim 1 wherein the level of gene transcription is determined for the genes having the nucleic acid sequences consisting of SEQ ID No.1, SEQ ID No.2, SEQ ID No.3, SEQ ID No.4, SEQ ID NO.5, SEQ ID NO.6, SEQ ID No.7, SEQ ID No.8, SEQ ID NO.9, SEQ ID 11, SEQ ID NO.13, SEQ ID NO.15, SEQ ID NO.17, SEQ ID NO.19, SEQ ID NO.21, SEQ ID NO.23, SEQ ID No.25, SEQ ID No.26, SEQ ID No.27, SEQ ID No.28, SEQ ID No.29, SEQ ID No.30, SEQ ID No.31, SEQ ID NO.32, SEQ ID NO.34, SEQ ID NO.36, SEQ ID No.38 and SEQ ID No.40.
4. (Currently Amended) A method according to ~~claims 1 or 2~~ claim 1 wherein the level of gene transcription is being assessed using a probe which binds to a polynucleotide comprising a nucleic acid sequence selected from the group consisting of SEQ ID No.1, SEQ ID No.2, SEQ ID No.3, SEQ ID No.4, SEQ ID NO.5, SEQ ID NO.6, SEQ ID No.7, SEQ ID No.8, SEQ ID NO.9, SEQ ID 11, SEQ ID NO.13, SEQ ID NO.15, SEQ ID NO.17, SEQ ID NO.19, SEQ ID NO.21, SEQ ID NO.23, SEQ ID No.25, SEQ ID No.26, SEQ ID No.27, SEQ ID No.28, SEQ ID No.29, SEQ ID No.30, SEQ

ID No.31, SEQ ID NO.32, SEQ ID NO.34, SEQ ID NO.36, SEQ ID No.38 and SEQ ID No.40.

5. (Currently Amended) A method according to ~~any one of claims 1 to 4~~ claim 1 wherein the level of gene expression is determined using microarray technology.
6. (Original) A method of diagnosing a CRH induced gene expression profile in an individual said method comprising;
 - a) obtaining a biological sample of said individual; and
 - b) determine the amount of at least one protein that modulates corticotropin releasing hormone (CRH) signaling in said biological sample; whereby the protein that modulates corticotropin releasing hormone (CRH) signaling is being selected from the group consisting of SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41.
7. (Original) A method according to claim 6 wherein the biological sample is a bodily fluid or tissue sample
8. (Currently Amended) A method according to ~~claims 6 or 7~~ claim 6 wherein wherein the amount of protein that modulates CRH signaling is being determined using an antibody which binds to a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41.
9. (Currently Amended) A method according to ~~claims 6 or 7~~ claim 6 wherein the amount of protein that modulates CRH signaling is being determined by assessing the level of gene transcription of a gene encoding an amino acid sequence selected from the group consisting of SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41.

10. (Original) A method according to claim 9 wherein the level of gene transcription is being assessed using a probe which binds to a polynucleotide encoding an amino acid sequence selected from the group consisting of SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41.
11. (Original) A method according to claim 10 wherein the level of gene expression is determined using microarray technology.
12. (Original) A method according to claim 11 wherein the level of gene transcription is analysed using an array of oligonucleotide probes that bind to the polynucleotides encoding the group of polypeptides having the amino acid sequences SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41.
13. (Original) A method according to claim 11 wherein the level of gene transcription is analysed using an array of oligonucleotide probes that bind to the polynucleotides having the nucleic acid sequences SEQ ID No.1, SEQ ID No.2, SEQ ID No.3, SEQ ID No.4, SEQ ID NO.5, SEQ ID NO.6, SEQ ID No.7, SEQ ID No.8, SEQ ID NO.9, SEQ ID 11, SEQ ID NO.13, SEQ ID NO.15, SEQ ID NO.17, SEQ ID NO.19, SEQ ID NO.21, SEQ ID NO.23, SEQ ID No.25, SEQ ID No.26, SEQ ID No.27, SEQ ID No.28, SEQ ID No.29, SEQ ID No.30, SEQ ID No.31, SEQ ID NO.32, SEQ ID NO.34, SEQ ID NO.36, SEQ ID No.38 and SEQ ID No.40.
14. (Original) A method for identifying a compound capable to alter the CRH signalling response in a cell, said method comprising;
 - a) contacting said cell with CRH in the presence and absence of said compound;
 - b) determine the amount of at least one protein that modulates corticotropin releasing hormone (CRH) signaling in said cell; and
 - c) compare the amount of said protein in the presence and absence of said compound;

whereby the protein that modulates corticotropin releasing hormone (CRH) signaling is being selected from the group consisting of SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41.

14. Canceled.
15. (Currently Amended) A method according to ~~claims 13 or 14~~ claim 13 wherein the amount of protein that modulates CRH signaling is being determined using an antibody which binds to a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41.
16. (Currently Amended) A method according to ~~claims 13 or 14~~ claim 13 wherein the amount of protein that modulates CRH signaling is being determined by assessing the level of gene transcription of a gene encoding an amino acid sequence selected from the group consisting of SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41.
17. (Original) A method according to claim 16 wherein the level of gene transcription is being assessed using a probe which binds to a polynucleotide encoding an amino acid sequence selected from the group consisting of SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41.
18. (Currently Amended) A method according to ~~claims 16 or 17~~ claim 16 wherein the level of gene expression is analysed using microarray technology.

19. (Original) A method according to claim 18 wherein the level of gene transcription is analysed using an array of oligonucleotide probes that bind to the polynucleotides encoding the group of polypeptides having the amino acid sequences SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41.
20. (Original) A method according to claim 18 wherein the level of gene transcription is analysed using an array of oligonucleotide probes that bind to the polynucleotides having the nucleic acid sequences SEQ ID No.1, SEQ ID No.2, SEQ ID No.3, SEQ ID No.4, SEQ ID NO.5, SEQ ID NO.6, SEQ ID No.7, SEQ ID No.8, SEQ ID NO.9, SEQ ID 11, SEQ ID NO.13, SEQ ID NO.15, SEQ ID NO.17, SEQ ID NO.19, SEQ ID NO.21, SEQ ID NO.23, SEQ ID No.25, SEQ ID No.26, SEQ ID No.27, SEQ ID No.28, SEQ ID No.29, SEQ ID No.30, SEQ ID No.31, SEQ ID NO.32, SEQ ID NO.34, SEQ ID NO.36, SEQ ID No.38 and SEQ ID No.40.
21. (Original) A method for identifying a compound capable to alter the CRH signalling response activity in a cell, said method comprising;
 - a) contacting a cell which expresses at least one protein comprising an amino acid sequence selected from the group consisting of SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41, with said test compound; and
 - b) compare the CRH response activity of said cell in the presence and absence of said compound.
22. (Original) A method according to claim 21 wherein the cell is a host cell capable to express at least one protein having an amino acid sequence selected from the group consisting of SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41.

23. (Original) A method according to claim 22 wherein the host cell is transfected with at least one vector comprising a regulatory sequence.
24. (Original) A method according to claim 22 wherein the host cell is transfected with at least one vector comprising a polynucleotide sequence encoding an amino acid sequence selected from the group consisting of SEQ ID NO.10, SEQ ID 12, SEQ ID NO.14, SEQ ID NO.16, SEQ ID NO.18, SEQ ID NO.20, SEQ ID NO.22, SEQ ID NO.24, SEQ ID NO.33, SEQ ID NO.35, SEQ ID NO.37, SEQ ID No.39 and SEQ ID No.41.
25. (Original) An isolated polynucleotide comprising a nucleic acid sequence selected from the group consisting of SEQ ID No.1, SEQ ID No.2, SEQ ID No.3, SEQ ID No.4, SEQ ID No.5, SEQ ID No.6, SEQ ID No.7, SEQ D No.8, SEQ ID No.25, SEQ ID No.26, SEQ ID No.27, SEQ ID No.28, SEQ ID No.29, SEQ ID No.30 and SEQ ID No.31, for use as a marker of CRH signaling in a cell.
26. (Original) An isolated polynucleotide according to claim 21 wherein said polynucleotide is mRNA, DNA or cDNA.
27. (Original) An isolated polynucleotide consisting of a nucleic acid sequence selected from the group consisting of SEQ ID No.1, SEQ ID No.2, SEQ ID No.3, SEQ ID No.4, SEQ ID No.5, SEQ ID No.6, SEQ ID No.7, SEQ D No.8, SEQ ID No.25, SEQ ID No.26, SEQ ID No.27, SEQ ID No.28, SEQ ID No.29, SEQ ID No.30 and SEQ ID No.31, for use as a marker of CRH signaling in a cell.
28. (Currently Amended) A vector comprising an isolated polynucleotide according to any one of claims 25 to 27 claim 25.
29. (Original) A vector according to claim 28 wherein the polynucleotide is operably linked to an expression control sequence.

30. (Currently Amended) A host cell transfected with a vector according to ~~claims 28 or 29~~ claim 28.
31. (New) A method according to claim 13 wherein the cell is a eukaryotic cell such as the murine pituitary corticotroph-derived adenoma cell line AtT-20.